Amendment to the Claims:

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 41 (Canceled)

Claim 42 (currently amended): A method of generating a variant nucleic acid encoding a polypeptide having a transaminase activity comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO:23, or a nucleic acid encoding a sequence as set forth in SEQ ID NO:31 ~~selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, 22, 23, and 39, sequences substantially identical thereto,~~ sequences complementary thereto, [[fragments]] sequences comprising at least 30 consecutive nucleotides thereof, and [[fragments]] sequences comprising at least 30 consecutive nucleotides of [[the]] sequences complementary to a sequence as set forth in SEQ ID NO:23 or a sequence encoding a polypeptide as set forth in SEQ ID NO:31 ~~SEQ ID NOS: 17, 18, 19, 20, 22, 23, and 39~~; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence to generate a variant nucleic acid encoding a polypeptide having a transaminase activity.

Claim 43 (currently amended): The method of claim 42, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in [[viva]] vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 44 (Original): The method of claim 42, wherein the modifications are introduced by error-prone PCR.

Claim 45 (Original): The method of claim 42, wherein the modifications are introduced by shuffling.

Claim 46 (Original): The method of claim 42, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Claim 47 (Original) The method of claim 42, wherein the modifications are introduced by assembly PCR.

Claim 48 (Original) The method of claim 42, wherein the modifications are introduced by sexual PCR mutagenesis.

Claim 49 (Original) The method of claim 42, wherein the modifications are introduced by in [[viva]] vivo mutagenesis.

Claim 50 (Original) The method of claim 42, wherein the modifications are introduced by cassette mutagenesis.

Claim 51 (Original) The method of claim 42, wherein the modifications are introduced by recursive ensemble mutagenesis.

Claim 52 (Original) The method of claim 42, wherein the modifications are introduced by exponential ensemble mutagenesis.

Claim 53 (Original) The method of claim 42, wherein the modifications are introduced by site-specific mutagenesis.

Claim 54 (Original) The method of claim 42, wherein the modifications are introduced by gene reassembly.

Claim 55 (currently amended) The method of claim 42, wherein the modifications are introduced by gene site saturated mutagenesis (GSSM™).

Claims 56 to 92 (Canceled)

Claim 93. (currently amended) A method of generating a variant nucleic acid encoding a polypeptide having a transaminase activity comprising:

obtaining a nucleic acid comprising (i) a sequence encoding a polypeptide having an aminotransferase activity and having at least 50% sequence identity to SEQ ID NO:31, or a nucleic acid having at least 50% sequence identity to SEQ ID NO:23 encoding a polypeptide having an aminotransferase activity ~~amino acid sequence selected from the group consisting of SEQ ID NOS:25, 26, 27, 28, 30, 31, and 40, sequences substantially identical thereto~~, (ii) sequences complementary thereto, [[fragments]] (iii) a sequence comprising at least 30 consecutive nucleotides of a sequence encoding a polypeptide having an aminotransferase activity and having at least 60% sequence identity to SEQ ID NO:31, or a nucleic acid having at least 60% sequence identity to SEQ ID NO:23 encoding a polypeptide having an aminotransferase activity, or [[thereof, and fragments]] (iv) a sequence comprising at least 30 consecutive nucleotides of [[the]] sequences complementary to (iii) ~~SEQ ID NOS:25, 26, 27, 28, 30, 31, and 40~~; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence to generate a variant nucleic acid encoding a polypeptide having a transaminase activity.

Claim 94 (currently amended): The method of claim 93, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in

[[viva]] vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 95 (new) A method of generating a variant nucleic acid encoding a polypeptide having a transaminase activity comprising:

obtaining a nucleic acid comprising (i) a sequence encoding a polypeptide having an aminotransferase activity and having at least 50% sequence identity to SEQ ID NO:31, or a nucleic acid having at least 50% sequence identity to SEQ ID NO:23 encoding a polypeptide having an aminotransferase activity, (ii) sequences complementary to (i), (iii) a sequence comprising at least 30 consecutive nucleotides of a sequence encoding a polypeptide having an aminotransferase activity and having at least 60% sequence identity to SEQ ID NO:31, or a nucleic acid having at least 60% sequence identity to SEQ ID NO:23 encoding a polypeptide having an aminotransferase activity, or (iv) a sequence comprising at least 30 consecutive nucleotides of sequences complementary to (iii);

generating modified sequences by modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence; and

screening the modified sequences for a variant nucleic acid encoding a polypeptide having a transaminase activity, thereby generating a variant nucleic acid encoding a polypeptide having a transaminase activity.

Claim 96 (new): The method of claim 95, wherein the polypeptide has at least 70% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 70% sequence identity to SEQ ID NO:23.

Claim 97 (new): The method of claim 96, wherein the polypeptide has at least 80% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 80% sequence identity to SEQ ID NO:23.

Claim 98 (new): The method of claim 97, wherein the polypeptide has at least 90% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 90% sequence identity to SEQ ID NO:23.

Claim 99 (new): The method of claim 98, wherein the polypeptide has at least 95% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 95% sequence identity to SEQ ID NO:23.

Claim 100 (new): The method of claim 99, wherein the polypeptide has at least 96% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 96% sequence identity to SEQ ID NO:23.

Claim 101 (new): The method of claim 100, wherein the polypeptide has at least 97% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 97% sequence identity to SEQ ID NO:23.

Claim 102 (new): The method of claim 101, wherein the polypeptide has at least 98% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 98% sequence identity to SEQ ID NO:23.

Claim 103 (new): The method of claim 102, wherein the polypeptide has at least 99% sequence identity to SEQ ID NO:31, or the nucleic acid has at least 99% sequence identity to SEQ ID NO:23.

Claim 104 (new): The method of claim 95, wherein the aminotransferase activity is a histidinol phosphate aminotransferase activity.